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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

Run on:

February 18, 2003, 09:20:45 ; Search time 48 Seconds
(without alignments)
5513.793 Million cell updates/sec

1 gcacgagetetateacacac.....aaaaaaaaaaaaaaaaaaaa 863 US-10-021-811-35 863 Title: Perfect score: Sequence:

OLIGO_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

441362 seqs, 153338381 residues

Searched:

9

Word size :

0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Issued_Patents_NA:*
1: /cgn2_6/ptodate31/ina/5A_COMB.seq:*
2: /cgn2_6/ptodate31/ina/5B_COMB.seq:*
3: /cgn2_6/ptodate31/ina/6A_COMB.seq:*
4: /cgn2_6/ptodate31/ina/6B_COMB.seq:*
5: /cgn2_6/ptodate31/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodate31/ina/PcTUS_COMB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ID Query Score Match Length DB Result

Description

No matches found

Search completed: February 18, 2003, 10:32:30 Job time : 48 secs

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Gaps

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Length 863; Indels

; DB 9; Lv 4.6e-301;

9

240

240

360

420

480 540 540 780

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TATTGCAAATCATGGGGAAGGTGTTTGGAACTCTTTGGCCAAAGCTGCTGGTCTCAAACG 180
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                                                                                                                                                                                       0; Mismatches
                                                                                                                                                        Score 863;
Pred. No. 4
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOFWARE: Microsoft Office 97
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAAAAAAAAAAAAAAA 863
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                                                                                                                                                          100.0%;
100.0%;
                                                                                                                                                                        Best_Local Similarity 100.
Matches 863; Conservative
                                                                           LENGTH: 863
TYPE: DNA
ORGANISM: Glycine max
US-10-021-811-35
                                                                                                                                                          Query Match
Best Local 8
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                                                                                                                       (without alignments)
7449.937 Million cell updates/sec
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                                                                                                                                                                                                      Search time 59 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_NA:*

| cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US07_BUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_BUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_BUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_BUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_BUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_BUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_BUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_BUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/pubpna/US10_pUBCOMB.seq:*/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /ptodata/1/pubpna/US10_NEW_PUB.seg:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Codell, Joan
APPLICANT: Odell, Joan
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REPERBENCE: BB1294 US MS
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
              5.1.3
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       863 9 US-10-021-811-35
                                                                                                                                                                                                                                                                                424239 segs, 254661826 residues
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              version - 2003
                                                                                                        February 18, 2003, 09:21:50
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                                                                         nucleic search, using sw model
                                                                                                                                                                                                                                OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Application US/10021811 Publication No. US20030024007A1 GENERAL INFORMATION:
              GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
                                                                                                                                                                   US-10-021-811-35
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Match Length DB
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Maximum DB seq
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9
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Description

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SUMMARIES

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                    Search completed: February 18, 2003, 10:02:37 Job time : 2196 secs
                                                        Query
Score Match Length DB
                                                                                                   No matches found
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کو
                                                                          February 18, 2003, 08:51:00 ; Search time 2196 Seconds
(without alignments)
11437.032 Million cell updates/sec
                                                                                                                                                Pred. No. is the number of results predicted by chance to have a
         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                      0
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                                                    OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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863
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February 18, 2003, 08:14:20 ; Search time 220 Seconds
    (without alignments)
    8833.975 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqn-embl_/NA1984.Ddf:*
| SIDS2/gcgdata/geneseq-geneseqn-embl_/NA1984.Ddf:*
| SIDS2/gcgdata/geneseq/geneseqn-embl_/NA1986.Ddf:*
| SIDS2/gcgdata/geneseq/geneseqn-embl_/NA1986.Ddf:*
| SIDS2/gcgdata/geneseq/geneseqn-embl_/NA1981.Ddf:*
| SIDS2/gcgdata/geneseq/geneseqn-embl_/NA1981.Ddf:*
| SIDS2/gcgdata/geneseq/geneseqn-embl_/NA1981.Ddf:*
| SIDS2/gcgdata/geneseq/geneseqn-embl_/NA1991.Ddf:*
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| SIDS2/gcgdata/geneseq/geneseqn-embl_/NA1999.Ddf:*
| SIDS2/gcgdata/geneseq/geneseqn-embl_/NA1999.Ddf:*
| SIDS2/gcgdata/geneseq/geneseqn-embl_/NA1999.Ddf:*
| SIDS2/gcgdata/geneseq/geneseqn-embl_/NA1999.Ddf:*
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| SIDS2/gcgdata/geneseq/geneseqn-embl_/NA2001.Ddf:*
| SIDS2/gcgdata/geneseq-embl_/NA20018.Ddf:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                          N_Geneseq_101002:*
.* /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
.* /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
.* /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2185239 seqs, 1125999159 residues
                                                                                                                                            OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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SUMMARIES

Description f Query Match Length DB Score

Result No.

No matches found

Search completed: February 18, 2003, 09:25:40 Job time : 221 secs

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/traislation="mdekgrslknnnmedemdlkropwtaeedfklmnytatnoegrw
NSLSRCAGLQRTGKSCRLRWLNYLRPDVRRGNITLEEQLLILELHSRWGNRWSKIAQY
LPGRTDNETKNYWRTRYQKHARQLICCDVNSQORDYRYTSLMMPRLOGSASASAA
AATTTTTTGSAGTSSCITTSNNOFMYDYNNNMGQOFGWSNNDYITPENSSASA
SPASOLTEYSABNDPEYXSQOMGNSYYPDQNLVSSQLLDEDNYBDYSGLLDEDLTAM
QEQSNLSWFENINGAASSSDSLWNIGETDEEFWFLQQQQQFNNNGSF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF262733 1423 bp mRNA linear PLN 30-AUG-2001
Arabidopsis thaliana putative transcription factor MYB108 (MYB108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosida; II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1423)
Stracke, R., Werber, M. and Weisshaar, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-MAY-2000) Biochemie, Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln D-50829, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stracke, R. and Weisshaar, B.
Stracke, R. and Weisshaar, B.
Direct Submission
Submitted (29-AUG-2001) Dept. Plant Breeding and Yield Physiology,
Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg
Max-Planck-Institut fuer Succhtungsforschung, Carl-von-Linne-Weg
Sequence update by submitter
On Aug 30, 2001 this sequence version replaced gi:8101955.
244 TATTACACCCGAGGAACAACTTTTGATTATGGAGCTCCACGCAAAGTGGGGGAAACAGGTG 303
                                                                                                                                 304 GTCCAAAATTGCCAAGCATCTACCTGGAAGGACTGATAATGAGATCAAGAGTATTGGAG 363
                                                                                                                                                                        373 TATCACACTCGAAGAACAGCTTCTCATTCTTGAACTCCATTCTCGTTGGGGCAATAGGTG 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative transcription factor MYB108" /protein_id="AAF72668.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="alternative transcription start site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The R2R3-WYB gene family in Arabidopsis thaliana Curr. Opin. Plant Biol. 4 (5), 447-456 (2001) 21481677
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                                                                                                                                                                                                                                                                      364 GACAAGGATCCAGAAGCACATCAAGCA 390
                                                                                                                                                                                                                                                                                                          493 AACGAGGGTCCAAAAACATGCCAAACA 519
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Stracke, R. and Weisshaar, B.
Direct Submission
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/gene="MYB108"
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AF262733
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                                                                                                                                                                                   Craterostigma plantagineum myb-related transcription factor (cpm7) mRNA, complete cds. 033917.1 GI:1002799
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/note-"putative DNA-binding protein; Description: myb-like
gene; myb-related transcription factor"
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AATUDDAAPPLASSASESAMWYACY STAMAAGDHRRQFKIJMQY YAWTHSNIMIA
QENSSTVA SSESTEGSLSSELTEMY ANYHQY I NGADHQQIDSSTTTSY GWQNDPAINY
VGNNGNSDQLGMGSVDDRRSNEQWAMADDVDNGGSSDKDNNLLWNVDDVWFLQQPSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A family of novel myb-related genes from the resurrection plant craterostidma blantagineum are specifically expressed in callus and roots in response to ABA or desiccation
Plant Mol. Biol. 32 (4), 707-716 (1996)
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HHGEGRWNSLARFAGLKRFGKSCRLRWLNYLRPDVRRGNITLEEQLLILELHSRWGNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Agenatophyta; Agenatophyta; Asteridae; core eudicots; Asteridae; euasterida I; Lamiales; Lamiales incertae sedis; Torenieae; Craterostigma.

Torenieae; Craterostigma.

Topasa; 1 to 1295)

Iturilaga, G., Leyns, L., Villegas, A., Gharaibeh, R., Salamini, F. and 'Bartels, D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11111111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 1
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/db_xref="taxon:4153"
1. 1295
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/db_xref="G1:1002800"
                                450 AACAAGGGTCCAAAAACATGCCAAACA 476
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125, .1132
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Watches 232; Conservative
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Direct Submission
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